

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 23, 2002, 14:37:43 ; Search time 27.3 Seconds
(without alignments)
1184.984 Million cell updates/sec

Title: US-09-811-118-1
Perfect score: 963
Sequence: 1 MVATVAAMLLMAACAQ.....VRLQITLVKRLILKREDL 187

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:.*
1: sp-archaea:.*
2: sp-bacteria:.*
3: sp-fungi:.*
4: sp-human:.*
5: sp-invertebrate:.*
6: sp-mammal:.*
7: sp-mhc:.*
8: sp-organelle:.*
9: sp-phage:.*
10: sp-plant:.*
11: sp-rodent:.*
12: sp-virus:.*
13: sp-vertebrate:.*
14: sp-unclassified:.*
15: sp-rylous:.*
16: sp-bacteriap:.*
17: sp-archaeap:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	964	98.1	187	4	Q96SL4	Q96SL4 homo sapien
2	871.5	88.7	186	11	Q99LJ6	Q99LJ6 mus musculu
3	830.5	84.5	225	11	Q9CXN6	Q9CXN6 mus musculu
4	601	61.1	147	11	Q9D111	Q9D111 mus musculu
5	508	51.7	209	11	Q9D7B7	Q9D7B7 mus musculu
6	358.5	36.5	159	16	Q97IS0	Q97IS0 clostridium
7	354	36.0	160	16	Q9A7J3	Q9A7J3 caulobacter
8	343	34.9	169	10	Q486A6	Q486A6 arabidopsis
9	343	34.9	232	10	Q94BV3	Q94BV3 arabidopsis
10	341	34.7	244	10	Q651S6	Q651S6 zantedeschia
11	337	34.3	170	10	Q9LEF0	Q9LEF0 mesembryant
12	337	34.0	237	10	Q9SME6	Q9SME6 hordeum vul
13	334	34.0	236	10	Q24296	Q24296 pisum sativ
14	331	33.7	236	8	O19985	O19985 arabidopsis
15	331	33.7	236	10	O81717	O81717 arabidopsis
16	330	33.6	230	10	Q9S254	Q9S254 arabidopsis

17	324	33.0	171	10	Q23814	Q23814 spinacia ol
18	323	32.9	165	10	Q9SME4	Q9SME4 hordeum vul
19	320.5	32.6	169	10	Q04922	Q04922 arabidopsis
20	320.5	32.6	173	10	Q9LYB4	Q9LYB4 arabidopsis
21	318	32.3	169	10	Q9FEV2	Q9FEV2 oryza sativ
22	315	32.0	158	16	Q92D38	Q92D38 listeria in
23	314	31.9	188	5	Q45183	Q45183 caenorhabd
24	313	31.8	197	6	Q9N2J2	Q9N2J2 bos taurus
25	312	31.7	206	10	Q22850	Q22850 arabidopsis
26	308	31.3	170	11	Q9JK35	Q9JK35 mus musculu
27	307	31.2	169	10	Q9FXS3	Q9FXS3 mus musculu
28	303.5	30.9	181	2	Q9LCQ9	Q9LCQ9 paenibacill
29	303	30.8	170	11	Q9JHM1	Q9JHM1 cavia porce
30	303	30.8	171	10	Q9SME5	Q9SME5 hordeum vul
31	302.5	30.8	181	16	Q97IU1	Q97IU1 clostridium
32	302.5	30.8	181	16	Q97IR9	Q97IR9 clostridium
33	302	30.7	171	10	Q9SLB6	Q9SLB6 arabidopsis
34	299	30.4	169	10	Q24031	Q24031 lycopersico
35	298.5	30.4	160	16	Q915A2	Q915A2 pseudomonas
36	298.5	30.4	170	10	Q49069	Q49069 gossypium h
37	296	30.1	197	11	Q35560	Q35560 mus musculu
38	296	30.1	257	11	Q91XR8	Q91XR8 rattus norv
39	295.5	30.1	194	16	Q9PDD0	Q9PDD0 xyella fas
40	295	30.0	192	10	Q9SH32	Q9SH32 arabidopsis
41	292	29.7	161	16	Q91017	Q91017 pseudomonas
42	291	29.6	253	11	Q91XR9	Q91XR9 mus musculu
43	283	28.8	167	2	Q9Z3H0	Q9Z3H0 synchococc
44	275.5	28.0	163	10	Q9SXL6	Q9SXL6 chlamydomon
45	273.5	27.8	158	16	Q99UG8	Q99UG8 staphylococ

ALIGNMENTS

RESULT 1
ID Q96SL4 PRELIMINARY; PRT; 187 AA.
AC Q96SL4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CDNA FLJ14777 FIS, CLONE NT2RP400259, WEAKLY SIMILAR TO
DE GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Iisogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahara K., Masuko Y., Sasaki N.,
RT "NEO human cDNA sequencing project."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027683; BAB5294.1; -
SQ SEQUENCE 187 AA; 20996 MW; 0ACB80AC2522EFCDC CRC64;

Query Match 98.1%; Score 964; DB 4; Length 187;
Best Local Similarity 98.9%; Pred. No. 1.6e-94;
Matches 185; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MVATVAAMLLMAACAQOBDPFDKRVNIRGKIVSLEKRGSVSLVNVASGEGT 60
DB 1 MVATVAAMLLMAACAQOBDPFDKRVNIRGKIVSLEKRGSVSLVNVASGEGT 60
QY 61 DQYRALQOQLORDLCPHFNFVLAFCNPGQPPDSNKELESFACRTYSVPMFSKIAV 120
DB 61 DQYRALQOQLORDLCPHFNFVLAFCNPGQPPDSNKELESFACRTYSVPMFSKIAV 120
QY 121 TGTGAHPAFKYLQTSKKEPTNNFMKYLVAADGKVVGVAMPDVSVEBRLQITLVKRLI 180
DB 121 TGTGAHPAFKYLQTSKKEPTNNFMKYLVAADGKVVGVAMPDVSVEBRLQITLVKRLI 180

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Db 121 TGTGAHPAFKYLAQTSGKEPTNFMFKYLVAADGKVVGAMPDPTVSVEEVRPQTALVAKLI 180
QY 181 LTKREDL 187
    |||||
Db 181 LTKREDL 187

RESULT 2
099LJ6 PRELIMINARY; PRT; 186 AA.
ID 099LJ6
AC 099LJ6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SMILAR TO RIKEN CDNA 3110050F08 GENE.
GN 3110050F08RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR. MAP-TGF ALPHA MODEL. 7 MONTHS OLD. GROSS
RC TISSUE;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC003228; AAH03228.1; -.
DR HSSP: P00435; 1GPI.
DR MGD: MGI:1914555; 3110050F08RIK.
DR InterPro: IPR000889; Glut_peroxidase.
DR Pfam: PF00255; GSHpx; 1.
DR PRINTS: PR01011; GLUTPEROXDASE.
DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
DR SEQUENCE 186 AA; 21061 MW; D20211218380A1BA CRC64;

Query Match 88.7%; Score 871.5; DB 11; Length 186;
Best Local Similarity 89.3%; Pred. No. 1,1e-84;
Matches 167; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 1 MVAATVAANLLMAAACAOQEDFYDFKAVNIRGKLVSEKRGSVSLVNVNASECGFT 60
    |||||
Db 1 MVAATVAANLLMAAACAOQEDFYDFKAVNIRGKLVSEKRGSVSLVNVNASECGFT 59

QY 61 DOHYRALQQLQRLDGRPHFNVLAFPCNQGQEPDNNKEIESFACRTYSVSPMFESKIV 120
    |||||
Db 60 DOHYRALQQLQRLDGRPHFNVLAFPCNQGQEPDNNKEIESFACRTYSVSPMFESKIV 119

QY 121 TGTGAHPAFKYLAQTSGKEPTNFMFKYLVAADGKVVGAMPDPTVSVEEVRPQTALVAKLI 180
    |||||
Db 120 TGTGAHPAFKYLAQTSGKEPTNFMFKYLVAADGKVVGAMPDPTVSVEEVRPQTALVAKLI 179

QY 181 LTKREDL 187
    |||||
Db 180 LTKREDL 186

RESULT 3
09CXN6 PRELIMINARY; PRT; 225 AA.
ID 09CXN6
AC 09CXN6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 3110050F08RIK PROTEIN.
GN 3110050F08RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD;

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RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kono S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamija M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK014199; BAB29201.1; -.
DR HSSP: P00435; 1GPI.
DR MGD: MGI:1914555; 3110050F08RIK.
DR InterPro: IPR000889; Glut_peroxidase.
DR Pfam: PF00255; GSHpx; 1.
DR PRINTS: PR01011; GLUTPEROXDASE.
DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
DR SEQUENCE 225 AA; 25606 MW; F3D7CEA1B4D22E06 CRC64;

Query Match 84.5%; Score 830.5; DB 11; Length 225;
Best Local Similarity 90.8%; Pred. No. 3.2e-80;
Matches 157; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

QY 1 MVAATVAANLLMAAACAOQEDFYDFKAVNIRGKLVSEKRGSVSLVNVNASECGFT 60
    |||||
Db 1 MVAATVAANLLMAAACAOQEDFYDFKAVNIRGKLVSEKRGSVSLVNVNASECGFT 59

QY 61 DOHYRALQQLQRLDGRPHFNVLAFPCNQGQEPDNNKEIESFACRTYSVSPMFESKIV 120
    |||||
Db 60 DOHYRALQQLQRLDGRPHFNVLAFPCNQGQEPDNNKEIESFACRTYSVSPMFESKIV 119

QY 121 TGTGAHPAFKYLAQTSGKEPTNFMFKYLVAADGKVVGAMPDPTVSVEEVRPQTALVAKLI 173
    |||||
Db 120 TGTGAHPAFKYLAQTSGKEPTNFMFKYLVAADGKVVGAMPDPTVSVEEVRPQTALVAKLI 172

RESULT 4
09D111 PRELIMINARY; PRT; 147 AA.
ID 09D111
AC 09D111;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 3110050F08RIK PROTEIN.
GN 3110050F08RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kono S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

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RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Botfelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Winking L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK004091: BAB23164.1: -
 DR HSSP: P00435: 1GPI: 3110050F08RIK.
 DR MGD: MGI:1914553: 3110050F08RIK.
 DR InterPro: IPR000889: Glut_peroxidase.
 DR Pfam: PF00255: GSHpx: 1.
 DR PRINTS: PR01011: GLUTPROXDAE.
 DR PROSITE: PS00763: GLUTATHIONE_PEROXID_2: 1.
 DR PROSITE: PS00763: GLUTATHIONE_PEROXID_2: 1.
 SQ SEQUENCE 147 AA: 16185 MW: F20B1C56DE968135 CRC64:

Query Match 61.1%; Score 601; DB 11; Length 147;
 Best Local Similarity 73.8%; Pred. No. 4.8e-56;
 Matches 121; Conservative 9; Mismatches 14; Indels 20; Gaps 2;

QY 1 MVAATVAAAMLILMAAACQOEODFYDFKAVNIRKGLVLEKRGVSILVNVASCGFT 60
 DB 1 MVAATVAAAMLILMAAACQOEODFYDFKAVNIRKGLVLEKRGVSILVNVASCGFT 59
 QY 61 DOHYRALOOLORDLGPHEHNVLAFCPOGQOEPPDSNKEIESFACRTYSVSPFMSKIAV 120
 DB 60 DOHYRALOOLORDLGPHEHNVLAFCPOGQOEPPDSNKEIESFACRTYSVSPFMSKIAV 119
 QY 121 TGTGAHPAFKYLQTSCKEPTWNNFKYLVAPDGKVVGAMPDPTS 164
 DB 120 TGTGCPPC-----LQVPRNLRLGRSPGTS 144

RESULT 5
 ID Q9D7B7 PRELIMINARY; PRT: 209 AA.
 AC Q9D7B7;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE 2310016C16RIK PROTEIN.
 GN 2310016C16RIK.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=TONGUE;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai T., Shinsawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi S., Yamamoto I.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,
 RA Saito T., Okazaki Y., Gojoubi T., Bono H., Kasukawa T., Saito R.,
 RA Kodota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fieischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Botfelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Winking L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK009378: BAB6254.1: -
 DR HSSP: P00435: 1GPI: 3110016C16RIK.
 DR MGD: MGI:1916840: 2310016C16RIK.
 DR InterPro: IPR000889: Glut_peroxidase.
 DR Pfam: PF00255: GSHpx: 1.
 DR PRINTS: PR01011: GLUTPROXDAE.
 DR PROSITE: PS00763: GLUTATHIONE_PEROXID_2: 1.
 DR PROSITE: PS00763: GLUTATHIONE_PEROXID_2: 1.
 SQ SEQUENCE 209 AA: 24148 MW: 8DA93ED1B4ECF21 CRC64:

Query Match 51.7%; Score 508; DB 11; Length 209;
 Best Local Similarity 49.7%; Pred. No. 5.9e-46;
 Matches 93; Conservative 37; Mismatches 55; Indels 2; Gaps 1;

QY 1 MVAATVAAAMLILMAAACQOEODFYDFKAVNIRKGLVLEKRGVSILVNVASCGFT 60
 DB 25 MVLCTVMT--FLQLKFLKPRINSFSEVDKAGRTVSLKFKKASLIVNVASDCRFT 82
 QY 61 DOHYRALOOLORDLGPHEHNVLAFCPOGQOEPPDSNKEIESFACRTYSVSPFMSKIAV 120
 DB 83 DKSQYTLRELHKEFGYHFNVLAFPCNOGSESEPKSSKEVSFAQNGVTPPIHKIKI 142
 QY 121 TGTGAHPAFKYLQTSCKEPTWNNFKYLVAPDGKVVGAMPDPTSVEVRLQITALVRKLI 180
 DB 143 LGPEAFAPRFLVDSKSKKPRNNFMKYLNVPEGQVVKFMRPEPLAIRPHVSOMIGIT 202
 QY 181 LKREDL 187
 DB 203 LKKEDEL 209

RESULT 6
 ID Q97IS0 PRELIMINARY; PRT: 159 AA.
 AC Q97IS0;
 DT 01-OCT-2001 (Tremblrel. 18, Created)
 DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE GLUTATHIONE PEROXIDASE.
 GN CAC1570.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Berton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hiltl J., Wolf Y.I.,
 RA Tatunov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum."
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL: AE007667: AAK79537.1: -
 DR InterPro: IPR000889: Glut_peroxidase.
 DR Pfam: PF00255: GSHpx: 1.
 DR PRINTS: PR01011: GLUTPROXDAE.
 DR PROSITE: PS00460: GLUTATHIONE_PEROXID_1: 1.
 DR PROSITE: PS00763: GLUTATHIONE_PEROXID_2: 1.
 KW Peroxidase; Complete proteome.
 SQ SEQUENCE 159 AA: 17931 MW: 8E5B78C07ED86CD4 CRC64;

Query Match 36.5%; Score 358.5; DB 16; Length 159;
 Best Local Similarity 45.2%; Pred. No. 3.3e-30;
 Matches 71; Conservative 26; Mismatches 55; Indels 5; Gaps 2;

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Db 4 YDFRAKDISGEISLSISKEGKVLIVNTASKGFTPO_YKLEEDIVYKLGNEKEILLGFP 62
QY 86 CNOGQOEPDSNKEISFACACTVSVPMSKIVNTGSGAMPARYIAQTS---GKEPT 141
Db 63 CNOGANDPBGSGIKNFCEINVTGTFLEFKIDVKGEMNAPLPRKYLASOGGILGKEIK 122
QY 142 WNFVKYLVAPDGKVVGAMPDPTVSVEVRLQITLALVR 178
Db 123 WNFVKFLDKKGVYVDRFAPYTKPSKTKDKYKLMEE 159

RESULT 7
ID 09A7J3 PRELIMINARY; PRT; 160 AA.
AC 09A7J3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
GN GLUTATHIONE PEROXIDASE.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=69394;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton R.J., Stephens C., Phade N.D., Ely B.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri M.L., Haft D.H.,
RA Ulteberg T., Tran K., Wolf A., Yamathavan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AB005847; AAK23706.1; -.
DR HSSP; P00435; 1GPI.
DR TIGR; CC1730; -.
DR InterPro: IPR000889; Glut_peroxidase.
DR Pfam; PF00255; GSHpx.1.
DR PRINTS; PR01011; GLUTPROXASE.
DR PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
KM Peroxidase; Complete proteome.
SQ SEQUENCE 160 AA; 17653 MW; 0180F8B07A06D731 CRC64;

Query Match 36.0%; Score 354; DB 16; Length 160;
Best Local Similarity 47.5%; Pred. No. 1e-29;
Matches 75; Conservative 25; Mismatches 48; Indels 10; Gaps 4;
QY 26 YDFKAVNIRKGLVSEKRGVSLVNVASGCGTDOH--YRALQOLRDLPFHFNLYA 83
Db 6 YDFSAKTLIDGQOVSLADYRGVLLVNTASKGFTPOYRGSLALYKAKHNDRG---FTYVLA 62
QY 84 FPCNPGQOEPDSNKEISFACACTVSVPMSKIVNTGSGAMPARYIAQTS---GKE 139
Db 63 FPCNPGQOEPDSNKEISFACACTVSVPMSKIVNTGSGAMPARYIAQTS---GKE 139
QY 140 P-TWNFVKYLVAPDGKVVGAMPDPTVSVEVRLQITLALVR 176
Db 123 P-TWNFVKYLVAPDGKVVGAMPDPTVSVEVRLQITLALVR 176

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DE GLUTATHIONE PEROXIDASE (EC 1.11.1.9).
GN TSC23.30 OR At4G11600.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98172218; PubMed=9511228;
RX Sugimoto M., Sakamoto W.;
RT "Putative phospholipid hydroperoxide glutathione peroxidase gene from
RT Arabidopsis thaliana induced by oxidative stress."
RL Genes Genet. Syst. 72:311-316(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LANDSBERG ERECTA;
RA Lers A., Burd S., Sonego L., Khalchitski A., Lomaniec E.;
RL Plant Physiol. 116:1193-1193(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-LANDSBERG ERECTA;
RA Bildeau P.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
RA Baneroff T., Kewes H.W., Mayer K.F.X., Scheller C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
RA Kewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROTECTS CELLS AND ENZYMES FROM OXIDATIVE DAMAGE. BY
CC CATALYSING THE REDUCTION OF HYDROGEN PEROXIDE. LIPID PEROXIDES AND
CC ORGANIC HYDROPEROXIDE, BY GLUTATHIONE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 2 GLUTATHIONE + H(2)O(2) = OXIDIZED
CC GLUTATHIONE + 2 H(2)O.
CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
CC ENCODED BY THE OPAL CODON, UGA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
DR EMBL; AB001568; BAA24226.1; -.
DR EMBL; AF030132; AAC09173.1; -.
DR EMBL; AL049500; CAB39931.1; -.
DR EMBL; AL161532; CAB78203.1; -.
DR HSSP; P00435; 1GPI.
DR ANO-ZDPAGE; 048646; -.
DR InterPro: IPR000889; Glut_peroxidase.
DR Pfam; PF00255; GSHpx.1.
DR PRINTS; PR01011; GLUTPROXASE.
DR PROSITE; PS00460; GLUTATHIONE_PEROXID_1; 1.
DR PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
DR Oxidoreductase; Peroxidase; Selenium; Selenocysteine.
FW BINDING 42 42 SELENIUM (BY SIMILARITY).
SQ SEQUENCE 169 AA; 18609 MW; E15F33A/FBB89DE4 CRC64;

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Query Match 34.9%; Score 343; DB 10; Length 169;
Best Local Similarity 42.3%; Pred. No. 1.6e-28;
Matches 71; Conservative 24; Mismatches 65; Indels 8; Gaps
QY 17 ACAQOEDDFDKAVNIRKGLVSEKRGVSLVNVASGCGTDOH-YRALQOLRDLP 76
Db 2 AASSEKSLYDFYKDAKGVYVDRFAPYTKPSKTKDKYKLMEE 159

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RP SEQUENCE FROM N.A.
RA Chouk R., Chen H., Kim C.J., Koeseema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Gibson H.A., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kanlaya A.,
RA Kerlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narisaka M., Nguyen M., Ondoca C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.,
RT "Arabidopsis cDNA clones.",
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY039863; AAK63967.1; -
SO SEQUENCE 232 AA; 25584 MW; 93F3084A8A331494 CRC64;

RESULT	10
065156	
ID	065156
AC	065156;
DT	01-AUG-1998 (TREMBLrel. 07, Created)
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	GLUTATHIONE PEROXIDASE (EC 1.11.1.9).
GN	GPX.
OS	Zantedeschia aethiopica (White calla lily).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
OC	Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Zantedeschia.
OX	NCBI_TaxID=69721;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=LEAF;
RA	Lino-Neto T., Tavares R.M., Palme K., Pais M.S.S.;

Rt	"Nucleotide sequence of a cDNA encoding a glutathione peroxidase
Rt	(Accession No. AF053311) from Zantedeschia aethiopica (L.) Spreng.
Rt	(PGR98-185)." ;
RL	Plant Physiol. 118:1102-1102(1996).
CC	-1- FUNCTION: PROTECTS CELLS AND ENZYMES FROM OXIDATIVE DAMAGE, BY
CC	CATALYSING THE REDUCTION OF HYDROGEN PEROXIDE, LIPID PEROXIDES AND
CC	ORGANIC HYDROPEROXIDE, BY GLUTATHIONE (BY SIMILARITY).
CC	-1- CATALYTIC ACTIVITY: 2 GLUTATHIONE + H(2)O(2) = OXIDIZED
CC	GLUTATHIONE + 2 H(2)O.
CC	-1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
CC	ENCODED BY THE OPAL CODON, UGA (BY SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
DR	EMBL; AF053311; AAC78466.1; .
DR	HSSP; P00435; 1GPI.
DR	InterPro: IPR000889; Glut_peroxidase.
DR	Pfam; PF00255; GSHpx; 1.
DR	PRINTS; PR01011; GLUTPEPOXDASE.
DR	PROSITE; PS00460; GLUTATHIONE_PEROXID_1; 1.
DR	PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
KW	Oxidoreductase; Peroxidase.
SQ	SEQUENCE 244 AA; 26761 MW; B342803420E5B7F6 CRC64;
Oy	Query Match 34.7%; Score 341; DB 10; Length 244;
Db	Best Local Similarity 42.3%; Pred.No.4.le=28;
	Matches 71; Conservative 24; Mismatches 65; Indels 8; Gaps 2;
Oy	17 ACAOEODFYEFKAVINIGKLVSLEKRGSVSLVNAVECGFTDOHRALOQLORDLGP 76
Db	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :
	79 ATAAEKRSIHDTFYVDIGDKRGSLSKFEGKULLIVNASRCGLTTSNMELSHIYEKKY 138
Oy	77 HHFNVLAFPCNOFGOEPPDSNKIESFACRTYSVSFPMSFKIAVTGAPHPAKYLAOTS 136
Db	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :
Oy	139 OGFEIIAFLPCNOFGSOEBEGTSEIKQFACTFGEKPFIFEDVDVNGPRTAPVOPLKSSA 198
Oy	137 ----GKEPTWNFWKYLVA PDGVKVGAMPPTYSV EVELRIOTALVALVKLI 180
Db	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :
	199 GGFLGDLLKWNFEKFLVDKNKGVERIPTTS----PQIEKDITKLIV 242
RESULT 11	
O9LEFO	PRELIMINARY; PRT; 170 AA.
AC	O9LEFO:
DT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE	GLUTATHIONE PEROXIDASE (EC 1.11.1.9).
GN	GPMXC1.
OS	Mesembryanthemum crystallinum (Common ice plant).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC	Caryophyllidae; Caryophyllales; Alzaoceae; Mesembryanthemum.
NM	NCBI_TaxId=3544;
[1]	
RP	SEQUENCE FROM N.A.
RC	TISSUE=LEAF;
RA	Kiefer M., Cushman J.C., Ratajczak R., Haag-Korner A.;
RT	"A putative phospholipid hydroperoxide glutathione peroxidase from the
RT	common ice plant Mesembryanthemum crystallinum." ;
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC	-1- FUNCTION: PROTECTS CELLS AND ENZYMES FROM OXIDATIVE DAMAGE, BY
CC	CATALYSING THE REDUCTION OF HYDROGEN PEROXIDE, LIPID PEROXIDES AND
CC	ORGANIC HYDROPEROXIDE, BY GLUTATHIONE (BY SIMILARITY).
CC	-1- CATALYTIC ACTIVITY: 2 GLUTATHIONE + H(2)O(2) = OXIDIZED
CC	GLUTATHIONE + 2 H(2)O.
CC	-1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
CC	ENCODED BY THE OPAL CODON, UGA (BY SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
DR	EMBL; AJ250951; CAB96145.1; .
DR	HSSP; P00435; 1GPI.
DR	InterPro: IPR000889; Glut_peroxidase.
DR	Pfam; PF00255; GSHpx; 1.

16 AACAAQEDDFDEFAVNIIRKRLYSLEKYGSSLYVNNAECGFTHDHYRALQQLQRDLG 75
 ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
 70 AAASSASVHDFVEDASCKVDLSTYKGKVLIIYNVASOGGLTNSNTETLAOLYERYK 125
 76 PHHFNVIAFPONQFGQQEPDSNKEISFACRTIYSVSPMFESKIANTVGGAHPARKYIAQT 135

[illegible]

RESULT	14	
01985		
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01-JAN-1998	(TIMBLrel, 05,	Created)
01-JAN-1998	(TIMBLrel, 05,	Last sequence update)
01-DEC-2001	(TIMBLrel, 19,	Last annotation update)

DE GLUTATHIONE PEROXIDASE (EC 1.11.1.9).
 GN GPXL.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=98345965; PubMed=9680987;
 RA Mullineaux P.M., Karpinski S., Jimenez A., Cleary S.P., Robinson C.,
 RA Creissen G.P.;
 RT "Identification of cDNAs encoding plastid-targeted glutathione
 RT peroxidase".
 RL Plant J. 13:375-379(1998).
 CC -1- FUNCTION: PROTECTS CELLS AND ENZYMES FROM OXIDATIVE DAMAGE, BY
 CC CATALYSING THE REDUCTION OF HYDROGEN PEROXIDE, LIPID PEROXIDES AND
 CC ORGANIC HYDROPEROXIDE, BY GLUTATHIONE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 GLUTATHIONE + H(2)O(2) -> OXIDIZED
 CC GLUTATHIONE + 2 H(2)O.
 CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
 CC ENCODED BY THE OPAL CODON, UGA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
 DR EMBL: AJ000469; CA04112.1; -.
 DR HSSP: P00435; IGPI.
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHpx.1.
 DR PRINTS: PR01011; GLUTPROXDAE.
 DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
 DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
 KW Chloroplast; Oxidoreductase; Peroxidase.
 SO SEQUENCE 236 AA; 26016 MW; D676C0381526C37A CRC64;

Query Match 33.7%; Score 331; DB 8; Length 236;
 Best Local Similarity 41.3%; Pred. No. 4.6e-27;
 Matches 69; Conservative 23; Mismatches 65; Indels 10; Gaps 2;

OY 17 ACAQOQODYDFKAVNIRKIVSLEKRGVSILVNVASCGFTDHYRALQQLORDLGP 76
 DB 71 ARAAAKTYVDFKVDIDGDAVNLNFKGKVMILVNVASCGFTSSNSLSLYEKRYT 130
 OY 77 HHNVLAFCNPGQOEPDSNKEIESFACRTYSVSPFMSKIAVGTGAPAFKYLQTS 136
 DB 131 QGEFIIAFCNPGQEPDSNKEIKQFACRTFAEPFIPKVVNGSTAPIEFLKSN 190
 OY 137 G-----KEPTWNEFKYLVAPDGKVVGAMPPTVSVEEVLQITALY 176
 DB 191 GGLGLGLIK---WNFEKFLDKKGVKVERYPPTSPFQIEKDIOKLL 234

RESULT 15
 ID 081717 PRELIMINARY; PRT; 236 AA.
 AC 081717;
 DT 01-NOV-1998 (TREMREL. 08, Created)
 DT 01-NOV-1998 (TREMREL. 08, Last sequence update)
 DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
 DE GLUTATHIONE PEROXIDASE (EC 1.11.1.9) (PUTATIVE GLUTATHIONE
 DE PEROXIDASE).
 GN AT2G25080.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Bentlo M.-I., Town C.D.,

RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., VanAken S.E., Unayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carreira A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhagen G.P., Preuss D., Nierman W.C., White O., Eilen J.A.,
 RA Salberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana".
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G.,
 RA Bowser L., Carolin P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
 RA Jones T., Kamuya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E.,
 RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,
 RA Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene F13d.40/Atg25080 (GI:6623873)".
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROTECTS CELLS AND ENZYMES FROM OXIDATIVE DAMAGE, BY
 CC CATALYSING THE REDUCTION OF HYDROGEN PEROXIDE, LIPID PEROXIDES AND
 CC ORGANIC HYDROPEROXIDE, BY GLUTATHIONE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 GLUTATHIONE + H(2)O(2) -> OXIDIZED
 CC GLUTATHIONE + 2 H(2)O.
 CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
 CC ENCODED BY THE OPAL CODON, UGA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
 DR EMBL: AC018722; AF19214.1; -.
 DR EMBL: AT035153; AK59657.1; -.
 DR HSSP: P00435; IGPI.
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHpx.1.
 DR PRINTS: PR01011; GLUTPROXDAE.
 DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
 DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
 KW Oxidoreductase; Peroxidase.
 SO SEQUENCE 236 AA; 26016 MW; D676C0381526C37A CRC64;

Query Match 33.7%; Score 331; DB 10; Length 236;
 Best Local Similarity 41.3%; Pred. No. 4.6e-27;
 Matches 69; Conservative 23; Mismatches 65; Indels 10; Gaps 2;

OY 17 ACAQOQODYDFKAVNIRKIVSLEKRGVSILVNVASCGFTDHYRALQQLORDLGP 76
 DB 71 ARAAAKTYVDFKVDIDGDAVNLNFKGKVMILVNVASCGFTSSNSLSLYEKRYT 130
 OY 77 HHNVLAFCNPGQOEPDSNKEIESFACRTYSVSPFMSKIAVGTGAPAFKYLQTS 136
 DB 131 QGEFIIAFCNPGQEPDSNKEIKQFACRTFAEPFIPKVVNGSTAPIEFLKSN 190
 OY 137 G-----KEPTWNEFKYLVAPDGKVVGAMPPTVSVEEVLQITALY 176
 DB 191 GGLGLGLIK---WNFEKFLDKKGVKVERYPPTSPFQIEKDIOKLL 234

Search completed: August 23, 2002, 14:39:40
 Job time: 117 sec

